

Patent Application US/08/029,330

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: Burkly, Linda C.

(ii) TITLE OF INVENTION: Treatment for Insulin Dependent Diabetes

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Allegretti & Witcoff, Ltd.

(B) STREET: 10 South Wacker Drive, Suite 3000

(C) CITY: Chicago

(D) STATE: IL

(E) COUNTRY: US

(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 9 February 1993

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McNicholas, Janet M.

(B) REGISTRATION NUMBER: 32,918

(C) REFERENCE/DOCKET NUMBER: 92,749; D015 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-715-1000

(B) TELEFAX: 312-715-1234

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
chain variable region; amino acid 1 is Glu (E) but Gln (Q)

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53 may be substituted"

54

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 1..360

58

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60

61	GTC	AAA	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AAG	CCA	GGG	GCC	TCA	48
62	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
63	2				6					11					16		
64																	
65	GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	ACC	TAT	96
66	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
67				21					26					31			
68																	
69	ATG	CAC	TGG	GTG	AAG	CAG	AGG	CCT	GAA	CAG	GGC	CTG	GAG	TGG	ATT	GGA	144
70	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
71			36					41					46				
72																	
73	AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	CCG	AAG	TTC	CAG	192
74	Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	Pro	Lys	Phe	Gln	
75		51					56					61					
76																	
77	GTC	AAG	GCC	ACT	ATT	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	240
78	Val	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Trp	Leu	
79	66					71					76					81	
80																	
81																	
82	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	288
83	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
84					86					91					96		
85																	
86	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	TTC	TGG	GGC	CAA	336
87	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	Trp	Gly	Gln	
88				101					106					111			
89																	
90	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA									360
91	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
92			116					121									
93																	

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105 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
106 2 6 11 16
107
108 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
109 21 26 31
110
111 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
112 36 41 46
113
114 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
115 51 56 61
116
117 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
118 66 71 76 81
119
120 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
121 86 91 96
122
123 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
124 101 106 111
125
126 Gly Thr Thr Val Thr Val Ser Ser
127 116 121
128

129 (2) INFORMATION FOR SEQ ID NO:3:

130

131 (i) SEQUENCE CHARACTERISTICS:

132 (A) LENGTH: 318 base pairs

133 (B) TYPE: nucleic acid

134 (C) STRANDEDNESS: double

135 (D) TOPOLOGY: linear

136

137 (ii) MOLECULE TYPE: cDNA

138

139 (ix) FEATURE:

140 (A) NAME/KEY: CDS

141 (B) LOCATION: 1..318

142 (D) OTHER INFORMATION: /product= "HP1/2 light chain
143 variable region"

144

145 (ix) FEATURE:

146 (A) NAME/KEY: misc_feature

147 (B) LOCATION: 1

148 (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
149 chain variable region"

150

151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

152

153 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA
154 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
155 1 5 10 15
156

48

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157 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96
158 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
159 20 25 30
160
161 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144
162 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
163 35 40 45
164
165 TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
166 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
167 50 55 60
168
169 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240
170 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
171 65 70 75 80
172
173 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288
174 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
175 85 90 95
176
177 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC 318
178 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
179 100 105
180
181 (2) INFORMATION FOR SEQ ID NO:4:
182
183 (i) SEQUENCE CHARACTERISTICS:
184 (A) LENGTH: 106 amino acids
185 (B) TYPE: amino acid
186 (D) TOPOLOGY: linear
187
188 (ii) MOLECULE TYPE: protein
189
190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
191
192 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
193 1 5 10 15
194
195 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
196 20 25 30
197
198 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
199 35 40 45
200
201 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
202 50 55 60
203
204 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
205 65 70 75 80
206
207 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
208 85 90 95

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209
210 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
211 100 105
212
213 (2) INFORMATION FOR SEQ ID NO:5:
214
215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 429 base pairs
217 (B) TYPE: nucleic acid
218 (C) STRANDEDNESS: single
219 (D) TOPOLOGY: linear
220
221 (ii) MOLECULE TYPE: cDNA
222
223 (ix) FEATURE:
224 (A) NAME/KEY: sig_peptide
225 (B) LOCATION: 1..57
226
227 (ix) FEATURE:
228 (A) NAME/KEY: mat_peptide
229 (B) LOCATION: 58..429
230
231 (ix) FEATURE:
232 (A) NAME/KEY: CDS
233 (B) LOCATION: 1..429
234
235 (ix) FEATURE:
236 (A) NAME/KEY: misc_feature
237 (B) LOCATION: 1
238 (D) OTHER INFORMATION: /note= "pBAG195 insert: AS heavy
239 chain variable region"
240
241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
242
243 ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT 48
244 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
245 -19 -15 -10 -5
246
247 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 96
248 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
249 1 5 10
250
251
252 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT 144
253 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
254 15 20 25
255
256 AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT 192
257 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
258 30 35 40 45
259
260 GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC 240

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261 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
262 50 55 60
263
264 CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC 288
265 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
266 65 70 75
267
268 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC 336
269 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
270 80 85 90
271
272 TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC 384
273 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
274 95 100 105
275
276 TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429
277 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
278 110 115 120
279
280 (2) INFORMATION FOR SEQ ID NO:6:
281
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 143 amino acids
284 (B) TYPE: amino acid
285 (D) TOPOLOGY: linear
286
287 (ii) MOLECULE TYPE: protein
288
289 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
290
291 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
292 -19 -15 -10 -5
293
294 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
295 1 5 10
296
297 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
298 15 20 25
299
300 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
301 30 35 40 45
302
303
304 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
305 50 55 60
306
307 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
308 65 70 75
309
310 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
311 80 85 90
312

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313 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
314 95 100 105

315
316

317 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
318 110 115 120

319

320 (2) INFORMATION FOR SEQ ID NO:7:

321

322 (i) SEQUENCE CHARACTERISTICS:

323 (A) LENGTH: 386 base pairs

324 (B) TYPE: nucleic acid

325 (C) STRANDEDNESS: single

326 (D) TOPOLOGY: linear

327

328 (ii) MOLECULE TYPE: cDNA

329

330 (ix) FEATURE:

331 (A) NAME/KEY: sig_peptide

332 (B) LOCATION: 1..57

333

334 (ix) FEATURE:

335 (A) NAME/KEY: mat_peptide

336 (B) LOCATION: 58..386

337

338 (ix) FEATURE:

339 (A) NAME/KEY: CDS

340 (B) LOCATION: 1..386

341

342 (ix) FEATURE:

343 (A) NAME/KEY: misc_feature

344 (B) LOCATION: 1

345 (D) OTHER INFORMATION: /note= "pBAG198 insert: VK2 (SVMDY)
346 light chain variable region"

347

348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

349

350 ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT 48
351 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
352 -19 -15 -10 -5

353

354

355

356 GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
357 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
358 1 5 10

359

360 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG 144
361 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
362 15 20 25

363

364 ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG 192

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365 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
366 30 35 40 45
367
368 CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA 240
369 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
370 50 55 60
371
372 TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288
373 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
374 65 70 75
375
376 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC 336
377 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
378 80 85 90
379
380 TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG TG 386
381 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
382 95 100 105
383
384 (2) INFORMATION FOR SEQ ID NO:8:
385
386 (i) SEQUENCE CHARACTERISTICS:
387 (A) LENGTH: 128 amino acids
388 (B) TYPE: amino acid
389 (D) TOPOLOGY: linear
390
391 (ii) MOLECULE TYPE: protein
392
393 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
394
395 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
396 -19 -15 -10 -5
397
398 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
399 1 5 10
400
401 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
402 15 20 25
403
404 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
405 30 35 40 45
406
407
408 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
409 50 55 60
410
411 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
412 65 70 75
413
414 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
415 80 85 90
416

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417 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
418 95 100 105
419

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/029,330

DATE: 04/08/93
TIME: 07:46:22
S5136

LINE ERROR

ORIGINAL TEXT

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/029,330

DATE: 04/08/93
TIME: 07:46:22
S5136

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/029,330

DATE: 04/08/93
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CORRECTED TEXT